Package 'RBM'

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Title RBM: a R package for microarray and RNA-Seq data analysis

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Depends R (>= 3.2.0), limma, marray

Description Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression in Two-Color Microarrays and RNA-Seq data sets.

License GPL (>= 2)

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R topics documented:

`RBM-package` *RBM:a package for microarray and RNA-Seq data analysis*

Description

Use A Resampling-Based Empirical Bayes Approach to Assesse Differential Expression or Identifying differntially methylated loci in Two-Color Microarrays and RNA-Seq data sets. Significant features selected through RBM_T or RBM_F functions could be further used as input for pathway analysis or experimental vilidations.

Details

Package:	RBM
Type:	Package
Version:	0.99.0
Date:	2014-10-05
Depends:	R (>= 3.0.0), limma, marray
License:	GPL (>= 2)

Author(s)

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References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

See Also

The RBM_T and RBM_F functions defined in this package. The limma and marray packages.

Examples

```
normal_data <- matrix(rnorm(200*6), 200, 6)
mydesign <- c(0,0,0,1,1,1)
norm_result <- RBM_T(normal_data,mydesign,50,0.05)

unif_data <- matrix(runif(200*7, 0.10, 0.95), 200, 7)
mydesign2 <- c(0,0,0, 1,1,1,1)
unif_result <- RBM_T(unif_data,mydesign2,100,0.05)

normdata_F <- matrix(rnorm(200*9, 0, 2), 200, 9)
mydesign_F <- c(0, 0, 0, 1, 1, 1, 2, 2, 2)
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
normresult_F <- RBM_F(normdata_F, mydesign_F, aContrast, 100, 0.05)

unifdata_F <- matrix(runif(200*18, 0.15, 0.98), 200, 18)
mydesign2_F <- c(rep(0, 6), rep(1, 6), rep(2, 6))
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
unifresult_F <- RBM_F(unifdata_F, mydesign2_F, aContrast, 100, 0.05)
```

ovarian_cancer_methylation *ovarian cancer methylation example from United Kingdom Ovarian Cancer Population Study (UKOPS)*

Description

This data set contains DNA methylation level from 1000 DNA methylation loci in 8 randomly selected women with 4 ovarian cancer cases (pre-treatment) and 4 age-matched healthy controls.

Usage

```
ovarian_cancer_methylation
```

Format

A matrix containing 1000 rows and 8 columns with each row denoting a methyaltion locus and each column denoting a subject.

Value

The ovarian cancer methylation example data set contains the following information:

IlmnID	Name of DNA methylation loci
case	Ovarian cancer patients
control	Healthy controls

Source

NCBI GEO website with access number GSE19711

References

Teschendorff AE, Menon U, Gentry-Maharaj A, Ramus SJ et al. Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Res 2010 Apr;20(4):440-6. PMID: 20219944

RBM_F *RBM_F: a R function for microarray and RNA-Seq data analysis for designs with more than two groups*

Description

Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression in Two-Color Microarrays and RNA-Seq data sets for designs with more than two groups.

Usage

```
RBM_F(aData, vec_trt, aContrast, repetition, alpha)
```

Arguments

aData	The input data set with rows and columns denoting features and samples, respectively
vec_trt	A vector for group notation such as 1s denote treatment group and 0s denote control group
aContrast	A vector for contrast. For example: if we want to compare group 1 with group 0, group 2 with group 1, and group 2 with group 0, then the contrast vector will be ("X1-X0", "X2"-"X1", "X2-X0")
repetition	The number of resamplings used in the analysis. You could use 1000 or higher number
alpha	The signifiance level

Details

Combine resampling with empirical Bayes approach for Microarrays and RNA-Seq data analysis.

Value

RBM_F produces a named list with the following components:

ordfit_t	orignal t statistics
ordfit_pvalue	original p-values from lmFit and eBayes
ordfit_beta0	estimated mean for the control group
ordfit_beta1	estimated mean difference between treatment and control group
permutation_p	calculated p-values from permutation method based on resampled test statistics
bootstrap_p	calculated p-values from bootstrap method based on resampled test statistics

Author(s)

Dongmei Li and Chin-Yuan Liang

References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

See Also

The RBM_T function defined in this package. The limma and marray packages.

Examples

```
normdata_F <- matrix(rnorm(200*9, 0, 2), 200, 9)
mydesign_new <- c(0, 0, 0, 1, 1, 1, 2, 2, 2)
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
normresult_F <- RBM_F(normdata_F, mydesign_new, aContrast, 100, 0.05)

unifdata_F <- matrix(runif(200*18, 0.15, 0.98), 200, 18)
mydesign2_new <- c(rep(0, 6), rep(1, 6), rep(2, 6))
aContrast <- c("X1-X0", "X2-X1", "X2-X0")
unifresult_F <- RBM_F(unifdata_F, mydesign2_new, aContrast, 100, 0.05)
```

RBM_T *RBM_T: a R function for microarray and RNA-Seq data analysis for two-group comparisons*

Description

Use A Resampling-Based Empirical Bayes Approach to Assess Differential Expression or Identify differntially methylated loci in Two-Color Microarrays and RNA-Seq data sets.

Usage

```
RBM_T(aData, vec_trt, repetition, alpha)
```

Arguments

aData	The input data set with rows and columns denoting features and samples, respectively
vec_trt	A vector for group notation such as 1s denote treatment group and 0s denote control group
repetition	The number of resamplings used in the analysis. You could use 1000 or higher number
alpha	The signifiance level

Details

Combine resampling with empirical Bayes approach for Microarrays and RNA-Seq data analysis.

Value

RBM_T produces a named list with the following components:

ordfit_t	orignal t statistics
ordfit_pvalue	original p-values from lmFit and eBayes
ordfit_beta0	estimated mean for the control group
ordfit_beta1	estimated mean difference between treatment and control group
permutation_p	calculated p-values from permutation method based on resampled test statistics
bootstrap_p	calculated p-values from bootstrap method based on resampled test statistics

Author(s)

Dongmei Li and Chin-Yuan Liang

References

Li D, Le Pape MA, Parikh NI, Chen WX, Dye TD (2013) Assessing Differential Expression in Two-Color Microarrays: A Resampling-Based Empirical Bayes Approach. PLoS ONE 8(11): e80099. doi: 10.1371/journal.pone.0080099

See Also

The RBM_F function defined in this package. The limma and marray packages.

Examples

```
normal_data <- matrix(rnorm(200*6), 200, 6)
mydesign <- c(0,0,0,1,1,1)
norm_result <- RBM_T(normal_data,mydesign,50,0.05)

unif_data <- matrix(runif(200*7, 0.10, 0.95), 200, 7)
mydesign2 <- c(0,0,0, 1,1,1,1)
unif_result <- RBM_T(unif_data,mydesign2,100,0.05)
```

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